

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2001, 10:52:24 ; Search time 47.29 Seconds
(without alignments)
12.392 Million cell updates/sec

Title: US-09-288-719-1
Perfect score: 28
Sequence: 1 GGGGS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organellar:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	17	2	09R4Y9
2	28	100.0	17	5	P82617
3	28	100.0	17	11	064450
4	28	100.0	20	2	09R582
5	28	100.0	23	4	09UC00
6	28	100.0	26	10	042226
7	28	100.0	37	5	09TMM2
8	28	100.0	40	4	013832
9	28	100.0	40	4	013833
10	28	100.0	64	10	09LNS5
11	28	100.0	65	12	09G5J8
12	28	100.0	66	5	09XZ08
13	28	100.0	66	6	09XT04
14	28	100.0	66	10	09SK19
15	28	100.0	67	10	042070
16	28	100.0	67	12	09G5J6
17	28	100.0	74	5	09VGC4
18	28	100.0	74	10	09LNS8
19	28	100.0	78	10	09SK01

20	28	100.0	80	10	09SUF7	09SUF7 arabidopsis
21	28	100.0	81	5	09VJ51	09VJ51 drosophila
22	28	100.0	82	10	004130	004130 lycopersico
23	28	100.0	83	10	09M714	09M714 zea mays (m
24	28	100.0	85	5	044629	044629 caenorhabd
25	28	100.0	87	10	09LR15	09LR15 pisum sativ
26	28	100.0	93	10	09SX10	09SX10 arabidopsis
27	28	100.0	94	5	09VSP7	09VSP7 drosophila
28	28	100.0	97	10	09LX6	09LX6 arabidopsis
29	28	100.0	98	10	09LMP9	09LMP9 oryza sativ
30	28	100.0	99	13	09YHM9	09YHM9 glinglymosto
31	28	100.0	100	3	09P5U9	09P5U9 neurospora
32	28	100.0	100	11	09R0P8	09R0P8 mus musculu
33	28	100.0	102	5	062385	062385 caenorhabd
34	28	100.0	102	5	09VYX2	09VYX2 drosophila
35	28	100.0	104	10	080985	080985 arabidopsis
36	28	100.0	108	10	065397	065397 arabidopsis
37	28	100.0	108	12	084375	084375 human parvo
38	28	100.0	108	12	084376	084376 human parvo
39	28	100.0	108	12	084382	084382 human parvo
40	28	100.0	108	12	084383	084383 human parvo
41	28	100.0	108	12	084384	084384 human parvo
42	28	100.0	108	12	084385	084385 human parvo
43	28	100.0	110	2	09ZA70	09ZA70 yerinia en
44	28	100.0	110	2	044555	044555 anabaena va
45	28	100.0	111	10	09LH11	09LH11 arabidopsis

ALIGNMENTS

RESULT 1
ID 09R4Y9 PRELIMINARY; PRT; 17 AA.
AC 09R4Y9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AROMATIC AMINE DEHYDROGENASE BETA SUBUNIT (FRAGMENT).
OS Alcalligenes faecalis.
OC Bacteria; Proteobacteria; beta subdivision; Alcalligenaceae;
OC Alcalligenes.
OX NCBI_TaxID=511;
RN [1]
RP SEQUENCE.
RX MEDLINE=94245619; PubMed=8188594;
RA Govindaraj S., Eisenstein E., Jones L.H., Sanders-Loehr J.,
RA Chistoserdov A.Y., Davidson V.L., Edwards S.L.;
RT "Aromatic amine dehydrogenase, a second tryptophan tryptophylquinone
enzyme".
RL J. Bacteriol. 176:2922-2929(1994).
SQ SEQUENCE 17 AA; 1510 MW; 6EEFEAB9D9D2661 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
Db 2 GGGGS 6

RESULT 2
ID P82617 PRELIMINARY; PRT; 17 AA.
AC P82617;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PYROKININ-5 (PEA-PK-5) (FXPRIL-AMIDE).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_Taxid=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RX TISSUE-ABDOMINAL PERISYMPATHETIC ORGANS;
 RC MEDLINE-99212469; PubMed-10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE-20189894; PubMed-10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of EXPRLamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -1- TISSUE SPECIFICITY: MAINLY IN ABDOMINAL PERISYMPATHETIC ORGANS AND
 TO A LESSER EXTENT IN RETROCEBERAL COMPLEX.
 CC -1- MASS SPECTROMETRY: MW-1651.7; METHOD-MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR INTERPRO: IPR001484;
 DR PROSITE: PS00539; PYROKININ; UNKNOWN_1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 17
 SQ SEQUENCE 17 AA; 1653 MW; 8527162EA5BBA54 CRC64;

Query Match 100.0%; Score 28; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 DB 1 GGGGS 5

RESULT 3
 ID 064450 PRELIMINARY; PRT; 17 AA.
 AC 064450;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE URIDINE MONOPHOSPHATE KINASE (EC 2.7.1.46) (URIDINE KINASE) (URIDINE
 DE MONOPHOSPHOKINASE) (FRAGMENT).
 GN UMPK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RA Ropp P.A., Traut T.W.;
 RT Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + URIDINE -> ADP + UMP.
 DR EMBL; U57332; AAB01998.1;
 DR MGD; MGI:98904; Umpk.
 KW Transferase.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1464 MW; 14E427CBA1168634 CRC64;

DB 5 GGGGS 9

RESULT 4
 ID 09R582 PRELIMINARY; PRT; 20 AA.
 AC 09R582;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TRANSFERIN-BINDING PROTEIN 2 (FRAGMENT).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_Taxid=487;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-93307625; PubMed-8319886;
 RA Griffiths E., Stevenson P., Byfield P., Ala'Adeen D.A.,
 RA Borriello S.P., Holland J., Parsons T., Williams P.;
 RT "Antigenic relationships of transferrin-binding proteins from
 Neisseria meningitidis, N. gonorrhoeae and Haemophilus influenzae;
 RT cross-reactivity of antibodies to NH2-terminal peptides.";
 RL FEMS Microbiol. Lett. 109:85-91(1993).
 DR INTERPRO: IPR001677;
 DR PFM; PF01298; Lipoprotein_5; 1.
 SQ SEQUENCE 20 AA; 1977 MW; 6000EE169F09227E CRC64;

Query Match 100.0%; Score 28; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 DB 3 GGGGS 7

RESULT 5
 ID 09UC00 PRELIMINARY; PRT; 23 AA.
 AC 09UC00;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENHANCEMENT OF WOUND HEALING PROCESS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pierschbacher M.D., Polarek J.W., Craig W.S., Tschopp J.F.,
 RA Sipes N.J., Harper J.R.,
 RL J. Cell. Biochem. 56:150-154(1994).
 SQ SEQUENCE 23 AA; 2268 MW; CE7399CB9903891 CRC64;

Query Match 100.0%; Score 28; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 DB 11 GGGGS 15

Query Match 100.0%; Score 28; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 DB 11 GGGGS 5

RESULT 6
 ID 042226 PRELIMINARY; PRT; 26 AA.
 AC 042226;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)

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DE SEED MATURATION PROTEIN (FRAGMENT).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DRY SEEDS OF A. THALIANA ECOTYPE COLUMBIA;
RA Raynal M., Grellier F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z29850; CAA82818.1; -.
FT NON_TER 1 1
SQ SEQUENCE 26 AA: 2370 MW: 660902E39464466A CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
DB 11 GGGGS 15

RESULT 7
O9TMM2 PRELIMINARY; PRT; 37 AA.
AC O9TMM2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DIPTERICIN HOMOLOG (FRAGMENT)
OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestrioidae; Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7386;
RN [1]
RP SEQUENCE.
RC TISSUE=LARVAL HEMOLYMPH;
RX MEDLINE=93074996; PubMed=1445217;
RA Ishikawa M., Kubo T., Natori S.;
RT "Purification and characterization of a dipterin homolog from
RT Sarcophaga peregrina (Flesh fly).";
RL Biochem. J. 287:573-578(1992).
CC -1- FUNCTION: BACTERICIDAL ACTIVITY AGAINST GRAM-NEGATIVE BACTERIA
CC E. COLI AND S. SONNEI.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED BY THE FAT BODY AND IS SECRETED
CC INTO THE HEMOLYMPH.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN THE LARVAE STARTS A FEW MINUTES
CC AFTER THE INJURY OF THE BODY WALL, REACHING A MAXIMUM AFTER ABOUT
CC 10 HOURS. THE MAXIMUM LASTS FOR AT LEAST 3 HOURS.
CC -1- INDUCTION: IN RESPONSE TO INJURY OF THE BODY WALL OF THE LARVAE.
KW Insect immunity; Antibiotic.
FT DOMAIN 18 22
FT NON_TER 37 37
SQ SEQUENCE 37 AA: 3928 MW: E3BAC8105D2DABC7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 5; Length 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
DB 19 GGGGS 23

RESULT 8
O13832 PRELIMINARY; PRT; 40 AA.
AC O13832:

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DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE B2 BRADYKININ RECEPTOR BASAL PROMOTER, ALLELE BP-58-C (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96209920; PubMed=8655154;
RA Braun A., Maier E., Kammerer S., Mueller B., Roscher A.A.;
RT "A novel sequence polymorphism in the promoter region of the human B2-
RT bradykinin receptor gene.";
RL Hum. Genet. 97:688-689(1996).
DR EMBL: X91663; CAA62851.1; -.
FT NON_TER 1 1
FT VARIANT 18 18 T -> I.
FT NON_TER 40 40
SQ SEQUENCE 40 AA: 4140 MW: 3908E9AD371EF4A5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 4; Length 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
DB 6 GGGGS 10

RESULT 9
O13833 PRELIMINARY; PRT; 40 AA.
AC O13833:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE B2 BRADYKININ RECEPTOR BASAL PROMOTER, ALLELE BP-58-T (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96209920; PubMed=8655154;
RA Braun A., Maier E., Kammerer S., Mueller B., Roscher A.A.;
RT "A novel sequence polymorphism in the promoter region of the human B2-
RT bradykinin receptor gene.";
RL Hum. Genet. 97:688-689(1996).
DR EMBL: X91664; CAA62852.1; -.
FT NON_TER 1 1
FT VARIANT 18 18 T -> T.
FT NON_TER 40 40
SQ SEQUENCE 40 AA: 4152 MW: 1408E9AD371EB17F CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 4; Length 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
DB 6 GGGGS 10

RESULT 10
O9LNS5 PRELIMINARY; PRT; 64 AA.
AC O9LNS5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

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DE T20H2.25 PROTEIN.
 GN T20H2.25.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA.
 RA Sakano H., Vaysberg M., Lee J.M., Lenz C., Liu S., Pham P.,
 RA Toriumi M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hong B., Liu A., Altati H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC T20H2 from Arabidopsis thaliana chromosome 1";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC022472; AAF79916.1; -
 SQ SEQUENCE 64 AA; 6017 MW; 7D7C534ED7AE93C2 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 64;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
 |||||
 DB 25 GGGGS 29

RESULT 11
 Q905J8 PRELIMINARY; PRT; 65 AA.
 AC Q905J8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
 DE CAPSID PROTEIN VP2 (FRAGMENT).
 OS Mink enteritis virus.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
 OX NCBI_TaxID=10792;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHEREPAHOV098;
 RA Tkachev S.Y., Mitrofanova E.E.;
 RT "Mink enteritis virus (Cherepanov098 isolate) VP2 gene 5'-region";
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF201476; AAF19379.1; -
 DR HSSP: P30129; 4DPV.
 DR INTERPRO: IPR001403; -
 DR PFAM: PF00740; Parvo_coat; 1.
 FT NON_TER 1
 FT NON_TER 65
 SQ SEQUENCE 65 AA; 6368 MW; CC4551C7B08EF08 CRC64;

Query Match 100.0%; Score 28; DB 12; Length 65;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
 |||||
 DB 27 GGGGS 31

RESULT 12
 Q9XZ08 PRELIMINARY; PRT; 66 AA.
 AC Q9XZ08;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, last annotation update)

DE CYCLIC AMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37)
 DE (FRAGMENT).
 GN KIN-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2.
 RA MEDLINE-99187058; PubMed-10085246;
 RA Tabish M., Clegg R.A., Rees H.H., Fisher M.J.;
 RT "Organization and alternative splicing of the Caenorhabditis elegans
 RT CAMP-dependent protein kinase catalytic-subunit gene (kin-1).";
 RL Biochem. J 338:209-216(1999).
 DR EMBL: AJ011936; CAB41353.1; -
 KW Kinase; Transferase.
 FT NON_TER 66
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 6808 MW; 42B0768BE947911 CRC64;

Query Match 100.0%; Score 28; DB 5; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
 |||||
 DB 11 GGGGS 15

RESULT 13
 Q9XT04 PRELIMINARY; PRT; 66 AA.
 AC Q9XT04;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
 DE T-COMPLEX POLYPEPTIDE 1 (FRAGMENT).
 GN TCPL.
 OS Macropus rufogriseus (Red-necked wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-99282512; PubMed-10353914;
 RA Shitani S., O'Huigin C., Toyosawa S., Michalova V., Klein J.;
 RT "Origin of gene overlap: the case of TCPL and ACAT2";
 RL Genetics 152:743-754(1999).
 DR EMBL: AF143499; AAD34977.1; -
 DR HSSP: P48425; 1A6D.
 DR INTERPRO: IPR002423; -
 DR PFAM: PR00118; cpn60_TCPL; 1.
 FT NON_TER 1
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7239 MW; 451A18AD520D60C CRC64;

Query Match 100.0%; Score 28; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
 |||||
 DB 50 GGGGS 54

RESULT 14
 Q9SK19 PRELIMINARY; PRT; 66 AA.
 AC Q9SK19;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, last annotation update)

DE AT2G10020 PROTEIN.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";
 RL Nature 402:761-768(1999).
 DR EMBL, AC006586; AAD22697.1;
 SQ SEQUENCE 66 AA; 6723 MW; 403DFD0812065919 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 DB 22 GGGGS 26

RESULT 15
 ID Q42070 PRELIMINARY; PRT; 67 AA.
 AC Q42070;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMblrel. 07, last annotation update)
 DE PROTEIN KINASE (FRAGMENT).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=WHOLE SEEDLINGS OF A. THALIANA ECOTYPE COLUMBIA;
 RA Hofte H.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL, Z26195; CAA81188.1;
 FT NON_TER 1
 SQ SEQUENCE 67 AA; 7304 MW; 9259577DA1124200 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 DB 47 GGGGS 51

Search completed: March 15, 2001, 11:10:52
 Job time: 1108 sec